

Genome**A.S.Olsen**

HIGH RESOLUTION CLONAL MAP OF CHROMOSOME 19p.
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A framework metric map of chromosome 19p was established by determining the order of, and distance between, 80 cosmids along the p-arm, using high resolution FISH to pronuclei (Brandriff et al., Genomics 23, 582-591, 1994). The sum of the distances between cosmids measured by pronuclear FISH indicated a minimum length of 18.8 Mb for the p-arm. Through a combination of cosmid fingerprinting, YAC STS screening and Alu-PCR hybridization, a total of 36 YAC/cosmid islands have been anchored to these FISH-ordered cosmids, and thereby incorporated into the metric map. These ordered clone islands cover a distance of 15.7 Mb, or 84% of the p-arm. Coverage at the cosmid level has been expanded by hybridization of ordered YACs to the cosmid library to identify additional cosmids/contigs underlying the YACs, and by extending cosmid contigs through hybridization walking. In some regions, cosmid coverage has been supplemented by screening BAC, PAC and P1 libraries. Most of the cosmid contigs in the ordered map have been analyzed by EcoRI mapping to validate contig assembly and to determine the length of the contigs. For bands p13.3-13.2-13.1 (14.8 Mb distance estimated by FISH), there are 83 EcoRI mapped cosmid contigs within the larger ordered YAC/cosmid islands. These EcoRI mapped contigs span 10.3 Mb, or 69% of the DNA in these bands. Over 150 STSs, including 42 highly polymorphic genetic markers, have been mapped to the p-arm. 114 of these STSs, including 36 genetic markers, have currently been incorporated into the ordered map. This gives an average density of one ordered STS every 175 kb. Over 55 unique genes and cDNAs, in addition to multiple members of the olfactory receptor gene family and zinc finger gene family, have been incorporated into the ordered map. This cosmid-based map affords a high level of resolution, on the order of 10 kb or less, and will provide the ideal starting material for large scale sequencing of chromosome 19p.

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